

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 14:56:34 ; Search time 413.564 Seconds  
(without alignments)  
10776.324 Million cell updates/sec

Title: US-09-625-573-3  
Perfect score: 1979  
Sequence: 1 CAGAGTCCTGAGACAGC.....ATATGCAATATAAAATTAG 1979

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002.\*  
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
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9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
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20: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1977.4	99.9	1979	16	Human monocytic che
2	1943.8	98.2	143068	21	Human low adenosin
3	1943.8	98.2	143068	21	Human low adenosin
4	1943.8	98.2	143068	21	Human adenosine re
5	1943.8	98.2	143068	21	Human adenosine re
6	1943.8	98.2	143068	24	Ovary cancer relat
7	1943.8	98.2	143068	21	Human adenosine re
8	1943.8	98.2	143068	21	Human low adenosin
9	1313	66.3	10528	24	Human immune syste

c	10	1286.4	65.0	10528	24	ABL323335
	11	1083	54.7	1083	22	AAS12140
	12	1081.4	54.6	1083	22	AAS12139
	13	1079.8	54.6	1083	23	ABI97976
	14	1078.2	54.5	1083	18	AAT96976
	15	980	49.5	2232	16	AAQ96297
	16	704.6	35.6	1059	18	AAT85163
	17	703.4	35.5	1225	19	AAT76920
	18	703.4	35.5	1225	22	ABA02317
	19	703.4	35.5	1225	22	AAH26903
	20	703.4	35.5	1477	18	AAT90117
	21	703.4	35.5	1477	22	AAF87099
	22	703.4	35.5	3383	18	AAT85161
	23	703.4	35.5	3383	21	AAF21271
	24	703.4	35.5	3383	21	AAA35149
	25	703.4	35.5	3383	22	AAD08577
	26	703.4	35.5	9141	24	ABA97318
	27	702	35.5	1376	20	AAV84126
	28	701.8	35.5	1225	24	ABA02318
	29	701.8	35.5	1414	22	AAF26390
	30	701.4	35.4	1059	22	AAI65463
	31	700.2	35.4	1414	18	AAT44042
	32	700.2	35.4	1414	21	AAT91481
	33	700.2	35.4	1414	22	AAD13181
	34	700.2	35.4	1414	22	AAD13282
	35	700.2	35.4	1414	24	ABK51853
	36	700	35.4	1059	19	AAV23992
	37	700	35.4	1059	24	ABA97319
	38	700	35.4	1071	20	AAV84125
	39	699.2	35.3	5674	20	AAZ24738
	40	697.6	35.3	1056	22	AAAD1398
	41	697.6	35.3	1056	22	AAAD13299
	42	697.6	35.3	1056	24	ABK51870
	43	696.8	35.2	1059	23	ABI97978
	44	692.2	35.0	1255	19	AAT76919
	45	683.4	34.5	1344	20	AAV84159

ALIGNMENTS

RESULT 1  
AAQ96298  
ID AAQ96298 standard; cDNA; 1979 BP.

XX AC AAQ96298;  
XX AC

XX DT 29-DEC-1995 (first entry)

XX DE Human monocytic chemoattractant protein-1 receptor MCP-1RB.

XX DE Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine; ss.

XX KW Homo sapiens.

XX OS Key Location/Qualifiers

XX FH CDS 81..1160

XX FT /\*tag= a

XX PN WO9519436-A.

XX XX 20-JUL-1995.

XX PD 11-JAN-1995; 95WO-US00476.

XX PF 13-JAN-1994; 94US-0182962.

XX PR (REGC ) UNIV CALIFORNIA.

XX PA Charo I, Coughlin S;

XX PI WPI; 1995-263866/34.

XX XX P-PSDB; AAR79166.

XX DR

XX

PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
PT for identifying antagonists and for treating diseases characterised by  
XX monocytic infiltrates

PS Disclosure; Fig 2; 84pp; English.

XX To identify and clone new members of the chemokine receptor gene  
CC family, degenerate oligo primers were designed corresp. to the  
CC conserved sequences R79167 in the second and R79168 in the third  
CC transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8  
CC receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293.  
CC The degenerate oligo incorporating EcoRI and XhoI sites at their 5',  
CC ends are Q96299 and Q96300. Amplification of cDNA derived from MM6  
CC cells with the primers yielded a number of PCR products. One cDNA  
CC appeared to encode a novel protein. To obtain a full-length version  
CC of this clone, a MM6 cDNA library was constructed in pPROG and probed  
CC with the PCR product. A 2.1 kb cDNA library was obtained. Analysis of  
CC additional clones in the MM6 cDNA library revealed a second  
CC sequence that was identical to the 2.1 kb cDNA sequence first obtained  
CC from the 5' UTR through the putative seventh transmembrane domain  
CC but contained a different cytoplasmic tail. The second sequence  
CC appears to represent an alternative splicing of the carboxyl-terminal  
CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA  
CC and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature  
CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB  
CC has a mol. wt. of about 41,000 daltons.

XX Sequence 1979 BP; 530 A; 434 C; 452 G; 563 T; 0 other;

Query Match 99.9%; Score 1977.4; DB 16; Length 1979;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGACTGCTGAGACAGCCACAGCTGAACAGAGAGAAAGTGGATTGAACAAGACGCAT 60

DB 1 CAGGAGTCTGCTGAGACAGCCACAGCTGAACAGAGAGAAAGTGGATTGAACAAGACGCAT 60

QY 61 TTCGCCAGTACATCCACACATGCTGTCCACATCTCGTCTCGGTTTATCAGAAATACCA 120

DB 61 TTCGCCAGTACATCCACACATGCTGTCCACATCTCGTCTCGGTTTATCAGAAATACCA 120

QY 121 ACGAGAGCGGTGAAGAAGTACACACTTTTGTGATTATGATTACGCTGCTCCCTGTTCATA 180

DB 121 ACGAGAGCGGTGAAGAAGTACACACTTTTGTGATTATGATTACGCTGCTCCCTGTTCATA 180

QY 181 AATTGACGTGAAGCAAAATGGGGCCCAACTCCTGCCCTCCGCTCTACTCGCTGGTGTCA 240

DB 181 AATTGACGTGAAGCAAAATGGGGCCCAACTCCTGCCCTCCGCTCTACTCGCTGGTGTCA 240

QY 241 TCTTTGGTTTGTGGGCAACATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300

DB 241 TCTTTGGTTTGTGGGCAACATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300

QY 301 AGTGCTTGACGTGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTA 360

DB 301 AGTGCTTGACGTGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTA 360

QY 361 CTCCTCCATTTGGGCTCACHCTGCTGCAATGAGTGGGTCTTTGGGAATGCAATGTGCA 420

DB 361 CTCCTCCATTTGGGCTCACHCTGCTGCAATGAGTGGGTCTTTGGGAATGCAATGTGCA 420

QY 421 AATTATTACAGAGGCTGTATCACATCGGTTATTTGGCGGAATCTCTTCATCATCTCC 480

DB 421 AATTATTACAGAGGCTGTATCACATCGGTTATTTGGCGGAATCTCTTCATCATCTCC 480

QY 481 TGACAAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTTGTCTTTAAAGCCAGGCGG 540

DB 481 TGACAAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTTGTCTTTAAAGCCAGGCGG 540

QY 541 TCACCTTTGGGTTGGTGCACAGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGG 600

DB 541 TCACCTTTGGGTTGGTGCACAGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGG 600

QY 601 CAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCCTGTTATGTCGTGGCCCTTATT 660

DB 601 CAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCCTGTTATGTCGTGGCCCTTATT 660

QY 661 TTCCACGAGGATGGAATAATTTCCACACAATAATGAGAAACATTTTCGGGCTGGTCTGC 720

DB 661 TTCCACGAGGATGGAATAATTTCCACACAATAATGAGAAACATTTTCGGGCTGGTCTGC 720

QY 721 CGCTGCTCATCATGTCATCTGCTACTCGGGAATCTCTGAAAGCCCTCTTCGGTGTGCGAA 780

DB 721 CGCTGCTCATCATGTCATCTGCTACTCGGGAATCTCTGAAAGCCCTCTTCGGTGTGCGAA 780

QY 781 ACGAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840

DB 781 ACGAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840

QY 841 TCTTCTGGACTCCCTTATAACATTTGCTCTCTGCTGAAACCTTCCAGGAATTTCTTCGGCC 900

DB 841 TCTTCTGGACTCCCTTATAACATTTGCTCTCTGCTGAAACCTTCCAGGAATTTCTTCGGCC 900

QY 901 TGAGTAACTGTGAAAGCCAGCTCAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960

DB 901 TGAGTAACTGTGAAAGCCAGCTCAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960

QY 961 GGATGACTCACTGCTGCTCAATCCATCATCTATGCTCTGCTGAGGAGGAGGAGGAGGAGG 1020

DB 961 GGATGACTCACTGCTGCTCAATCCATCATCTATGCTCTGCTGAGGAGGAGGAGGAGGAGG 1020

QY 1021 GGTATCTCTCGGTGTTCTTCCGAAAGCACATCACCAGCGCTTCTGCAACAATGTCACG 1080

DB 1021 GGTATCTCTCGGTGTTCTTCCGAAAGCACATCACCAGCGCTTCTGCAACAATGTCACG 1080

QY 1081 TTTTCTACAGGAGACAGTGGATGAGTGACTTCAACAACAGCGCTTCCACATGGGGAGC 1140

DB 1081 TTTTCTACAGGAGACAGTGGATGAGTGACTTCAACAACAGCGCTTCCACATGGGGAGC 1140

QY 1141 AGGAAGTCTCGCTGCTGTTTATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200

DB 1141 AGGAAGTCTCGCTGCTGTTTATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200

QY 1201 TAACAATCTGTATATAACAACAACCTTCAAGGGTTTGTGAAACAATAGAAACCTGTAAAG 1260

DB 1201 TAACAATCTGTATATAACAACAACCTTCAAGGGTTTGTGAAACAATAGAAACCTGTAAAG 1260

QY 1261 CAGTGCCCGAGAACCTCAGGCTGTGTACTATAACAGAGACTATGTACCCCAATGTCATA 1320

DB 1261 CAGTGCCCGAGAACCTCAGGCTGTGTACTATAACAGAGACTATGTACCCCAATGTCATA 1320

QY 1321 TCCAAACATGTCTCAGGGAATAATCCAGAAAACCTGCTGGGTAGAGACTTTGACTCTCCAG 1380

DB 1321 TCCAAACATGTCTCAGGGAATAATCCAGAAAACCTGCTGGGTAGAGACTTTGACTCTCCAG 1380

QY 1381 AAAGCTCATCTCAGCTCCTGAAAATGCGCTCATTAACCTGTGCTAAATCCTCTTTTCTAG 1440

DB 1381 AAAGCTCATCTCAGCTCCTGAAAATGCGCTCATTAACCTGTGCTAAATCCTCTTTTCTAG 1440

QY 1441 TCTTCAATTTCTTCACTCAATCTGCTGATCTGCTCAATGCTTCAAAATGAGGCGGAGC 1500

DB 1441 TCTTCAATTTCTTCACTCAATCTGCTGATCTGCTCAATGCTTCAAAATGAGGCGGAGC 1500

QY 1501 TGGAGGTGAAGAAGAGAAATGTGACAGGCACAGATGAATGGGAGTGGGAGTGGGAGTGG 1560

DB 1501 TGGAGGTGAAGAAGAGAAATGTGACAGGCACAGATGAATGGGAGTGGGAGTGGGAGTGG 1560

QY 1561 AGGGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620

DB 1561 AGGGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620

QY 1621 GAGCAAGGGCTCACGATTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680

DB 1621 GAGCAAGGGCTCACGATTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680

QY 1681 GTGATTTAACTTCAAGGTTCCAGGTCAGGAGAGTTGGCAACTGCATTAACCTG 1740  
 |||||  
 Db 1681 GTGATTTAACTTCAAGGTTCCAGGTCAGGAGAGTTGGCAACTGCATTAACCTG 1740  
 |||||  
 QY 1741 GGAGTTTGGTGGAGTCCGATGATTTCTTTTGCATAAGTCATGACATATTTTGGCTTT 1800  
 |||||  
 Db 1741 GGAGTTTGGTGGAGTCCGATGATTTCTTTTGCATAAGTCATGACATATTTTGGCTTT 1800  
 |||||  
 QY 1801 ATTACAGTTTATCTATGACCCATGACCTTACATTTGAAATCTATGAATATCATGCT 1860  
 |||||  
 Db 1801 ATTACAGTTTATCTATGACCCATGACCTTACATTTGAAATCTATGAATATCATGCT 1860  
 |||||  
 QY 1861 CAAATGTTTCAGATGCTTTAGGCCACATCCCTGCTAAATAATTCAGAAAATTTTGT 1920  
 |||||  
 Db 1861 CAAATGTTTCAGATGCTTTAGGCCACATCCCTGCTAAATAATTCAGAAAATTTTGT 1920  
 |||||  
 QY 1921 TTATAAAGATCAATATCTATGATGCTAATATATATATGATGCAATATAAATTTAG 1979  
 |||||  
 Db 1921 TTATAAAGATCAATATCTATGATGCTAATATATATATGATGCAATATAAATTTAG 1979  
 |||||

RESULT 2  
 AAF21105  
 ID AAF21105 standard; DNA; 143068 BP.  
 XX  
 AC AAF21105;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenine antisense oligonucleotide related sequence #2672.  
 XX  
 KW Low adenine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200062736-A2.  
 PN  
 XX  
 XX 26-OCT-2000.  
 PD  
 XX  
 XX 24-MAR-2000; 2000WO-US08020.  
 PF  
 XX  
 XX 06-APR-1999; 99US-0127958.  
 PR  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 XX Nyce JW;  
 XX  
 XX WPI; 2000-679539/66.  
 DR  
 XX  
 XX Low adenine (A) content antisense oligonucleotides which do not  
 PT trigger adenine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 PT  
 XX  
 XX Disclosure; Page 924-957; 1592pp; English.  
 PS  
 XX  
 XX The present invention describes low adenine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and

CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 XX Sequence 143068 BP; 41194 A; 30122 C; 32403 G; 39349 T; 0 other;

Query Match 98.2%; Score 1943.8; DB 21; Length 143068;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 CTGAACAGAGAAAGTGGATTGAACAGGAGCGCATTTCCCCAGTACATCCACAAATCGT 86  
 |||||  
 Db 46052 CAGAACAGAGAAAGTGGATTGAACAGGAGCGCATTTCCCCAGTACATCCACAACTGCTG 46111  
 |||||  
 QY 87 TCCACATCTCTCTCTCGTTTATCAGAAATACCAACAGAGCGGTGAAGTCAACACC 146  
 |||||  
 Db 46112 TCCACATCTCTCTCTCGTTTATCAGAAATACCAACAGAGCGGTGAAGTCAACACC 46171  
 |||||  
 QY 147 TTTTGTGATATGATTAAGTACGGTGTCTCTGTCATAAATTTGACGTGAGCAAAATTTGGGCC 206  
 |||||  
 Db 46172 TTTTGTGATATGATTAAGTACGGTGTCTCTGTCATAAATTTGACGTGAGCAAAATTTGGGCC 46231  
 |||||  
 QY 207 CAACCTCGCTCGCGCTACTCGTGTCTATCTTTGTTTGTGGGCAACATGCTG 266  
 |||||  
 Db 46232 CAACCTCGCTCGCGCTACTCGTGTCTATCTTTGTTTGTGGGCAACATGCTG 46291  
 |||||  
 QY 267 GTGCTCTCTCATTTAATAAAGCTGCAAAAGCTGAAGTGCITTGACTGACATTTACTGCTC 326  
 |||||  
 Db 46292 GTGCTCTCTCATTTAATAAAGCTGCAAAAGCTGAAGTGCITTGACTGACATTTACTGCTC 46351  
 |||||  
 QY 327 AACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTTGTGGGCTCACTCTCCT 386  
 |||||  
 Db 46352 AACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTTGTGGGCTCACTCTCCT 46411  
 |||||  
 QY 387 GCAATGAGTGGGCTTTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCACATC 446  
 |||||  
 Db 46412 GCAATGAGTGGGCTTTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCACATC 46471  
 |||||  
 QY 447 GGTATTATTGGCGGAATCTTCTTCATCATCTCTCTGCAAAATCGATAGATACCTGCTATT 506  
 |||||  
 Db 46472 GGTATTATTGGCGGAATCTTCTTCATCATCTCTCTGCAAAATCGATAGATACCTGCTATT 46531  
 |||||  
 QY 507 GTCCATGCTGTGTTGCTTTTAAAGCCAGAGCGGTCACTTTGGGCTGGTGACAAAGTGTG 566  
 |||||  
 Db 46532 GTCCATGCTGTGTTGCTTTTAAAGCCAGAGCGGTCACTTTGGGCTGGTGACAAAGTGTG 46591  
 |||||  
 QY 567 ATCACTGTGTTGGGCTGTGTTGCTTCTGTCCAGGAATCATCTTTACTAAATGCCAG 626  
 |||||  
 Db 46592 ATCACTGTGTTGGGCTGTGTTGCTTCTGTCCAGGAATCATCTTTACTAAATGCCAG 46651  
 |||||  
 QY 627 AAAGAAGATCTGTTTATGCTGTGGCCCTTATTFTTCCAGAGATGGAATAATTTCCAC 686  
 |||||  
 Db 46652 AAAGAAGATCTGTTTATGCTGTGGCCCTTATTFTTCCAGAGATGGAATAATTTCCAC 46711  
 |||||  
 QY 687 ACAATAATGAGAAACAATTTTGGGCTGTGCTCTGCCGCTGCTCATCATGCTCATAC 746



Db 46772 TCGGGAATCCTGAAACCCCTGCTTCGGTGTCTCGAAACGAGAAGAGGCATAGGGCAGTG 46833

QY 1887 CATCCCTGCTCTAAATTCAGAAATTTGTTTATATAAAGATGCAATATCTATGATA 1946  
|||||  
Db 47912 CATCCCTGCTCTAAATTCAGAAATTTGTTTATATAAAGATGCAATATCTATGATA 47971  
|||||  
QY 1947 TGCTAATATATGATATGCAATATAA 1973  
|||||  
Db 47972 TGCTAATATATGATATGCAATATAA 47998  
|||||

## RESULT 4

AAA34983

ID AAA34983 standard; DNA; 143068 BP.

XX AC AAA34983;

XX DT 28-JUL-2000 (first entry)

XX DE Human adenosine receptor related polynucleotide SEQ ID NO:2672.

XX KW Human: adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antihistaminic; cytosolic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200009525-A2.

XX PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US17712.

XX PR 03-AUG-1998; 98US-0095212.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PI Nyce JW;

XX DR WPI; 2000-205971/18.

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers -

XX PS Disclosure; Page 851-882; 1343pp; English.

XX CC The present invention describes a new composition comprising an  
XX antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
XX targets nucleic acids involved in bronchoconstriction, allergies, and/or  
XX inflammation. The ON can have antiinflammatory, antiallergic,  
XX antiasthmatic, cytosolic and analgesic activities. The compositions are  
XX useful for the treatment of diseases associated with inflammation,  
XX impaired airways, including lung disease and diseases whose secondary  
XX effects afflict the lungs of a subject. They can be used for treating  
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
XX asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
XX pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
XX carcinomas, and cancers which may metastasize to the lungs, including  
XX breast and prostate cancer. The reduction of the adenosine content of  
XX the ONs reduces side effects. The A-containing ONs break down with the  
XX release of deoxyadenosine which activates adenosine receptors causing  
XX bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
XX nucleotide sequences given in the sequence listing from the present  
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
XX 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
XX differ from the previously named sequences. SEQ ID NO:11 to 1680  
XX (AAA32323 to AAA33992) are specifically claimed ONs from the present



[illegible]





OS Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.

XX 05-JUN-2000; 2000US-209531P.

XX 18-SEP-2000; 2000US-233133P.

XX 18-SEP-2000; 2000US-233617P.

XX 20-SEP-2000; 2000US-234009P.

XX 20-SEP-2000; 2000US-234034P.

XX 20-SEP-2000; 2000US-234052P.

XX 22-SEP-2000; 2000US-234509P.

XX 22-SEP-2000; 2000US-234567P.

XX 25-SEP-2000; 2000US-234923P.

XX 25-SEP-2000; 2000US-234924P.

XX 25-SEP-2000; 2000US-235077P.

XX 25-SEP-2000; 2000US-235082P.

XX 25-SEP-2000; 2000US-235134P.

XX 25-SEP-2000; 2000US-235280P.

XX 26-SEP-2000; 2000US-235637P.

XX 26-SEP-2000; 2000US-235638P.

XX 27-SEP-2000; 2000US-235711P.

XX 27-SEP-2000; 2000US-235720P.

XX 27-SEP-2000; 2000US-235840P.

XX 27-SEP-2000; 2000US-235863P.

XX 28-SEP-2000; 2000US-236028P.

XX 28-SEP-2000; 2000US-236032P.

XX 28-SEP-2000; 2000US-236033P.

XX 28-SEP-2000; 2000US-236034P.

XX 28-SEP-2000; 2000US-236109P.

XX 28-SEP-2000; 2000US-236111P.

XX 29-SEP-2000; 2000US-236842P.

XX 29-SEP-2000; 2000US-236891P.

XX 02-OCT-2000; 2000US-237172P.

XX 02-OCT-2000; 2000US-237173P.

XX 02-OCT-2000; 2000US-237278P.

XX 02-OCT-2000; 2000US-237294P.

XX 02-OCT-2000; 2000US-237295P.

XX 02-OCT-2000; 2000US-237316P.

XX 03-OCT-2000; 2000US-237425P.

XX 03-OCT-2000; 2000US-237598P.

XX 03-OCT-2000; 2000US-237604P.

XX 03-OCT-2000; 2000US-237606P.

XX 03-OCT-2000; 2000US-237608P.

XX 01-NOV-2000; 2000US-244867P.

XX 01-NOV-2000; 2000US-245084P.

XX (AVAL-) ANVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrihan S;

XX Soppet DR, Weaver Z;

XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a

XX chemical agent to be tested for anti-neoplastic activity, and

XX determining a change in expression of a gene of a signature gene set

XX Claim 1; SEQ ID 6461; 44pp; English.

XX The present invention describes a method (M1) for screening for an

XX anti-neoplastic agent. The method involves exposing cells to a chemical

XX agent to be tested for anti-neoplastic activity, determining a change in

XX expression of at least one gene (I) of a signature gene set, where (I)

XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664

XX to ABL70110), or is at least 95% identical to (S), where a change in

XX expression is indicative of anti-neoplastic activity. (I) has cytostatic

XX activity and can be used in gene therapy. M1 can be used for screening

XX an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a  
CC result of M1, and the data is sufficient to convey the chemical  
CC structure and/or properties of the agent. M1 can be used in the  
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 143068 BP; 41194 A; 30122 C; 32403 G; 39349 T; 0 Other;

Query Match 98.2%; Score 1943.8; DB 24; Length 143068;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 CTGAACAGAGAAAGTGGATTGAACAGGACGCAATTCCTCCAGTACATCCACACATGCTG 86

DB 46052 CAGAACAGAGAAAGTGGATTGAACAGGACGCAATTCCTCCAGTACATCCACACATGCTG 46111

QY 87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAAGAGAGCGGTGAAGAAGTCACACACC 146

DB 46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAAGAGAGCGGTGAAGAAGTCACACACC 46171

QY 147 TTTTGTGATTATGATTACGGTCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGGGGCC 206

DB 46172 TTTTGTGATTATGATTACGGTCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGGGGCC 46231

QY 207 CAATCTCGCTCCGCTCTACTCGGTGGTTCATCTTTGGTTTCTGGGCAACATGCTG 266

DB 46232 CAATCTCGCTCCGCTCTACTCGGTGGTTCATCTTTGGTTTCTGGGCAACATGCTG 46291

QY 267 GTCGCTCTCATCTTAATAAAGCTGCAAAAGCTGAAGTGTGACTGACATTTACCTGCTC 326

DB 46292 GTCGCTCTCATCTTAATAAAGCTGCAAAAGCTGAAGTGTGACTGACATTTACCTGCTC 46351

QY 327 AACCTGGCCATCTCTGATCTGCTTTTCTTATTTACTCTCCATTTGGGCTCACTCTGCT 386

DB 46352 AACCTGGCCATCTCTGATCTGCTTTTCTTATTTACTCTCCATTTGGGCTCACTCTGCT 46411

QY 387 GCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTACAGGGCTGTATCACATC 446

DB 46412 GCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTACAGGGCTGTATCACATC 46471

QY 447 GGTATTTTGGCGGAATCTTCTTCATCATCCTCTGACAAATCATAGATACCTGGCTATT 506

DB 46472 GGTATTTTGGCGGAATCTTCTTCATCATCCTCTGACAAATCATAGATACCTGGCTATT 46531

QY 507 GTCCATGCTGTGTTGCTTTAAAGCCAGGACGCTACCTTTGGGGTGTGACAAGTGTG 566

DB 46532 GTCCATGCTGTGTTGCTTTAAAGCCAGGACGCTACCTTTGGGGTGTGACAAGTGTG 46591

QY 567 ATCACCCTGGTGGTGGTGTGTTTGTCTGTCTCCAGGAATCATCTTTACTAAATGCCAG 626

DB 46592 ATCACCCTGGTGGTGGTGTGTTTGTCTGTCTCCAGGAATCATCTTTACTAAATGCCAG 46651

QY 627 AAAGAAGATTTCTGTTATGCTGTGGCCCTTATTTTCCAGGAGGATGAATAATTTCCAC 686

DB 46652 AAAGAAGATTTCTGTTATGCTGTGGCCCTTATTTTCCAGGAGGATGAATAATTTCCAC 46711

QY 687 ACAATAATGAGGACATTTTGGGCTGTCTGCTGCTGCTCATCTGCTCATCTGCTGCTAC 746

DB 46712 ACAATAATGAGGACATTTTGGGCTGTCTGCTGCTGCTCATCTGCTCATCTGCTGCTAC 46771

QY 747 TCGGGAATCTCTGAAACCCCTGCTTGGTGTGCGAAACGAGAGAGAGGAGGATAGGCGAGTG 806

DB 46772 TCGGGAATCTCTGAAACCCCTGCTTGGTGTGCGAAACGAGAGAGAGGAGGATAGGCGAGTG 46831

QY 807 AGAGTCATCTTCCACCATCATGATTGTTTACTTCTTCTGACTCCCTATAACATGCTC 866

DB 46832 AGAGTCATCTTCCACCATCATGATTGTTTACTTCTTCTGACTCCCTATAACATGCTC 46891

QY 867 ATTCTCTGACACCTTCCAGGAATTTCTGGGCTGTGAGTAACTGTGAAAGCAGCAGTCAA 926

DB 867 ATTCTCTGACACCTTCCAGGAATTTCTGGGCTGTGAGTAACTGTGAAAGCAGCAGTCAA 926

Db 46892 ATTCTCTGACACCTTCCAGGAATTCCTGGCCCTGAGTAACTGTGAAGACCACAGTCAA 46951  
QY 927 CTGGACCAAGCCAGCGAGGTGACAGAGACTTTGGGATGACTCACTGCTGCATCAATCCC 986  
Db 46952 CTGGACCAAGCCAGCGAGGTGACAGAGACTTTGGGATGACTCACTGCTGCATCAATCCC 47011  
QY 987 ATCATCTATGCTTCTGTTGGGAGAGTTTCAGAGGTATCTCTCGGTGTTCTCCGAAAG 1046  
Db 47012 ATCATCTATGCTTCTGTTGGGAGAGTTTCAGAGGTATCTCTCGGTGTTCTCCGAAAG 47071  
QY 1047 CACATCACCAGCGCTTCTGCAACAAATGTCAGTTTCTACAGGGAGACAGTGGATGGA 1106  
Db 47072 CACATCACCAGCGCTTCTGCAACAAATGTCAGTTTCTACAGGGAGACAGTGGATGGA 47131  
QY 1107 GTGACTTCAACAAACAGCGCTTCCACTGGGAGCAGGAAGTCTCGGTGTTTATAAAG 1166  
Db 47132 GTGACTTCAACAAACAGCGCTTCCACTGGGAGCAGGAAGTCTCGGTGTTTATAAAG 47191  
QY 1167 GAGGAGCAGTTGATGTTGTTTATAAAGGAGATACAAATCTGTATATAACAACAAT 1226  
Db 47192 GAGGAGCAGTTGATGTTGTTTATAAAGGAGATACAAATCTGTATATAACAACAAT 47251  
QY 1227 TCAAGGGTTGTTGAACATAGAAACCTGTAAAGCAGGTGCCAGGAACCTCAGGGCTGT 1286  
Db 47252 TCAAGGGTTGTTGAACATAGAAACCTGTAAAGCAGGTGCCAGGAACCTCAGGGCTGT 47311  
QY 1287 GTGTACTATACAGACTATGTACCAACATGCATATCCACATGTGTCAGGGAATATCC 1346  
Db 47312 GTGTACTATACAGACTATGTACCAACATGCATATCCACATGTGTCAGGGAATATCC 47371  
QY 1347 AGAAACCTGTGGGTAGAGACTTTGACTCTCCAGAAAGTCACTCAGTCTCTGAAAT 1406  
Db 47372 AGAAACCTGTGGGTAGAGACTTTGACTCTCCAGAAAGTCACTCAGTCTCTGAAAT 47431  
QY 1407 GCCTATTACCTTGCTGAATCCTCTTTTCTAGTCTTCATATTTCTTCACTCAATCTC 1466  
Db 47432 GCCTATTACCTTGCTGAATCCTCTTTTCTAGTCTTCATATTTCTTCACTCAATCTC 47491  
QY 1467 TGATCTGTCATGTCCTGAATCAAGGCCAGCTGGAGGTGAAGAGAAATGTGACAG 1526  
Db 47492 TGATCTGTCATGTCCTGAATCAAGGCCAGCTGGAGGTGAAGAGAAATGTGACAG 47551  
QY 1527 GCACAGATGAATGGGAGTGAGGATAGTGGGTGAGGCTGAGAGAGAGAGGAGAC 1586  
Db 47552 GCACAGATGAATGGGAGTGAGGATAGTGGGTGAGGCTGAGAGAGAGAGGAGAC 47611  
QY 1587 ATGAGCATGGCTGAGCCTGGACAAAGAGAGGTGAGCAAGGGCTCAGGCATTCAGCCA 1646  
Db 47612 ATGAGCATGGCTGAGCCTGGACAAAGAGAGGTGAGCAAGGGCTCAGGCATTCAGCCA 47671  
QY 1647 GGAGATGATGATGCTGCTTAGCCCATCTGCCACGTGATTTAACTTGAAGGGTTCACC 1706  
Db 47672 GGAGATGATGATGCTGCTTAGCCCATCTGCCACGTGATTTAACTTGAAGGGTTCACC 47731  
QY 1707 AGGTCAGGAGAGTTTGGGAACTGCAATATCACTGGAGCTTTGGTGGAGTCCGATGATTC 1766  
Db 47732 AGGTCAGGAGAGTTTGGGAACTGCAATATCACTGGAGCTTTGGTGGAGTCCGATGATTC 47791  
QY 1767 TCTTTTCATAGTCATGACATATTTTGTGTTTATACAGTTTATCATGATGATTC 1826  
Db 47792 TCTTTTCATAGTCATGACATATTTTGTGTTTATACAGTTTATCATGATGATTC 47851  
QY 1827 CACCTTACATTTGAAATCTATGAATATCATGCTCCATGTTTCAGATGCTTCTTAGGCCA 1886  
Db 47852 CACCTTACATTTGAAATCTATGAATATCATGCTCCATGTTTCAGATGCTTCTTAGGCCA 47911  
QY 1887 CATCCCTCTCAAAATTCAGAAATTTTGTGTTTATAAAGATGCAATATCATGATGATA 1946  
Db 47912 CATCCCTCTCAAAATTCAGAAATTTTGTGTTTATAAAGATGCAATATCATGATGATA 47971  
QY 1947 TGCTAATATATGATATGCAATATAA 1973  
Db 47972 TGCTAATATATGATATGCAATATAA 47998

## RESULT 7

AAA35151

ID AAA35151 standard; DNA; 149412 BP.

XX AAA35151;

XX 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:25.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
phosphorothioate; impaired respiration; inflammation; allergy;  
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;  
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary  
vasoconstriction, inflammation, allergies, asthma, hypertension, or  
bronchitis, emphysema, respiratory distress syndrome, ischemia or  
cancers

XX Disclosure; Page 1138-1171; 1343pp; English.

XX The present invention describes a new composition comprising an  
antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
targets nucleic acids involved in bronchoconstriction, allergies, and/or  
inflammation. The ON can have antiinflammatory, antiallergic,  
antiasthmatic, cytostatic and analgesic activities. The compositions are  
useful for the treatment of diseases associated with inflammation,  
impaired airways, including lung disease and diseases whose secondary  
effects afflict the lungs of a subject. They can be used for treating  
e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
carcinomas, and cancers which may metastasize to the lungs, including  
breast and prostate cancer. The reduction of the adenosine content of  
the ONs reduces side effects. The A-containing ONs break down with the  
release of deoxyadenosine which activates adenosine receptors causing  
bronchoconstriction and inflammation. AAA32313 to AAA35312 represent  
nucleotide sequences given in the sequence listing from the present  
invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
differ from the previously named sequences. SEQ ID NO:11 to 180  
(AAA32323 to AAA33992) are specifically claimed ONs from the present  
invention. N.B. Sequences given in the disclosure of the present  
invention do not match up with their corresponding SEQ ID NO: sequences  
given in the sequence listing.

XX Sequence 149412 BP; 43049 A; 31388 C; 33852 G; 41123 T; 0 other;

XX Query Match 98.2%; Score 1943.8; DB 21; Length 149412;

Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	27	CTGAACAGAGAAAGTGGATTGAACAAGAGCGCATTTCCCCAGTACATCCACAACATGCTG	86
Db	52396	CAGAACAGAGAAAGTGGATTGAACAAGAGCGCATTTCCCCAGTACATCCACAACATGCTG	52455
QY	87	TCACATCTCGTCTCGGTTTATCAGAAATACCACGAGAGCGGTGAGAGTCAACCACC	146
Db	52456	TCACATCTCGTCTCGGTTTATCAGAAATACCACGAGAGCGGTGAGAGTCAACCACC	52515
QY	147	TTTTTTGATTATGATTACGGTGTCTCCCTGTCATAAATTTGACGTGAAGCAAAATTTGGGGCC	206
Db	52516	TTTTTTGATTATGATTACGGTGTCTCCCTGTCATAAATTTGACGTGAAGCAAAATTTGGGGCC	52575
QY	207	CAACTCGCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTGTGTTGGGCAACATGCTG	266
Db	52576	CAACTCGCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTGTGTTGGGCAACATGCTG	52635
QY	267	GTGCTCTCATCTTAATAAAGCTCAAAAGCTGAAGTGTGACTGACATTTACCTGCTC	326
Db	52636	GTGCTCTCATCTTAATAAAGCTCAAAAGCTGAAGTGTGACTGACATTTACCTGCTC	52695
QY	327	AACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTTGGGGCTCACTCTGCT	386
Db	52696	AACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTTGGGGCTCACTCTGCT	52755
QY	387	GCAATAGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTATCACAGGGCTGTATCACATC	446
Db	52756	GCAATAGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTATCACAGGGCTGTATCACATC	52815
QY	447	GGTTATTTTGGCGGAATCTTCTTCATCATCTCTGCAATCGATAGATACCTGGCTATT	506
Db	52816	GGTTATTTTGGCGGAATCTTCTTCATCATCTCTGCAATCGATAGATACCTGGCTATT	52875
QY	507	GTCCATCTGTTTGTGTTTAAAGCCAGGACGGTCACTTTGGGGTGGTGACAAGTGTG	566
Db	52876	GTCCATCTGTTTGTGTTTAAAGCCAGGACGGTCACTTTGGGGTGGTGACAAGTGTG	52935
QY	567	ATCACCTGGTGGTGGTGTGTTGCTTGTGTCACGAGATCATCTTTACTAAATGCCAG	626
Db	52936	ATCACCTGGTGGTGGTGTGTTGCTTGTGTCACGAGATCATCTTTACTAAATGCCAG	52995
QY	627	AAAGAAGATCTGTTTATGCTGTGGCCCTTATTTTCCACGAGATGGAATAATTTCCAC	686
Db	52996	AAAGAAGATCTGTTTATGCTGTGGCCCTTATTTTCCACGAGATGGAATAATTTCCAC	53055
QY	687	ACAATAATGAGGAACATTTTGGGGTGGTCTGCTGCTGCTCATCTGTTCAATCTGCTAC	746
Db	53056	ACAATAATGAGGAACATTTTGGGGTGGTCTGCTGCTGCTCATCTGTTCAATCTGCTAC	53115
QY	747	TCGGGAATCTGAAACCCCTGCTTCGGTGTGCAACGAGAGAGAGGCGCATAGGCGATG	806
Db	53116	TCGGGAATCTGAAACCCCTGCTTCGGTGTGCAACGAGAGAGAGGCGCATAGGCGATG	53175
QY	807	AGAGTCACTTCCACATCATGATTGTTTACTTTCTCTCTGCTGCTCCCTATAAATTTGTC	866
Db	53176	AGAGTCACTTCCACATCATGATTGTTTACTTTCTCTCTGCTGCTCCCTATAAATTTGTC	53235
QY	867	ATTCTCTGAAACACCTTCCAGGAATTTTCGGCCCTGAGTAACATGTGAAAGCACCAGTCAA	926
Db	53236	ATTCTCTGAAACACCTTCCAGGAATTTTCGGCCCTGAGTAACATGTGAAAGCACCAGTCAA	53295
QY	927	CTGACCAAGCCAGCGAGTACAGAGACTCTTGGGATGACTCACTGCTGCTCAATCCC	986
Db	53296	CTGACCAAGCCAGCGAGTACAGAGACTCTTGGGATGACTCACTGCTGCTCAATCCC	53355
QY	987	ATCATCTATGCTTCTGTTGGGAGAGTTCAGAGGTATCTCTCGGTGTTCTCCGAAAG	1046
Db	53356	ATCATCTATGCTTCTGTTGGGAGAGTTCAGAGGTATCTCTCGGTGTTCTCCGAAAG	53415
QY	1047	CACATCACCAAGCGGTCTGCAAAACAAATGTCCAGTTTTTCTACAGGGAGACAGTGGATGGA	1106

Db	53416	CACATCACCAAGCGCTTCTGCAAAACAATGTCCAGTTTTTCTACAGGGAGACAGTGGATGGA	53475
QY	1107	GTGACTTCAACAACACAGCCCTTCCACTGGGAGCAGAGAGTCTCGGCTGTTTATAAATC	1166
Db	53476	GTGACTTCAACAACACAGCCCTTCCACTGGGAGCAGAGAGTCTCGGCTGTTTATAAATC	53535
QY	1167	GAGGAGCAGTTTGATTTCTGTTTATAAAGGAGATAACAATCTGTATATACAAACAAT	1226
Db	53536	GAGGAGCAGTTTGATTTCTGTTTATAAAGGAGATAACAATCTGTATATACAAACAAT	53595
QY	1227	TCAAGGGTGTGTTGAACAATAGAAAACCTGTAAAGCAGGTGCCAGGAACTTCAGGGCTGT	1286
Db	53596	TCAAGGGTGTGTTGAACAATAGAAAACCTGTAAAGCAGGTGCCAGGAACTTCAGGGCTGT	53655
QY	1287	GTGTACTTAATACAGACTATGTCCACCAATGCATATCCAAATGTGCTCAGGGAATAATCC	1346
Db	53656	GTGTACTTAATACAGACTATGTCCACCAATGCATATCCAAATGTGCTCAGGGAATAATCC	53715
QY	1347	AGAAAACTGTGGGTAGAGACTTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT	1406
Db	53716	AGAAAACTGTGGGTAGAGACTTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT	53775
QY	1407	GCCTCATACCTTGTGCTAATCCCTCTTTTCTAGTCTTCATTAATTTCTTCACTCAATCTC	1466
Db	53776	GCCTCATACCTTGTGCTAATCCCTCTTTTCTAGTCTTCATTAATTTCTTCACTCAATCTC	53835
QY	1467	TGATTTCTCAATCTCTTGAATCAAGGCCAGCTGGAGGTGAAGAAGAGATGTGACAG	1526
Db	53836	TGATTTCTCAATCTCTTGAATCAAGGCCAGCTGGAGGTGAAGAAGAGATGTGACAG	53895
QY	1527	GCACAGATGAATGGGAGTGGGATAGTGGGCTCAGGCTGAGAGGAGAGAGGAGAC	1586
Db	53896	GCACAGATGAATGGGAGTGGGATAGTGGGCTCAGGCTGAGAGGAGAGAGGAGAC	53955
QY	1587	ATGAGCATGGCTGAGCCTGGAGCAAGAGCAAGAGGTGAGCAAGGGCTCAGCATTCAGCCA	1646
Db	53956	ATGAGCATGGCTGAGCCTGGAGCAAGAGCAAGAGGTGAGCAAGGGCTCAGCATTCAGCCA	54015
QY	1647	GGAGATGATCTGCTGCTTACGCCCATCTGCCACGTGTATTTAACTTTGAAGGGTTCACC	1706
Db	54016	GGAGATGATCTGCTGCTTACGCCCATCTGCCACGTGTATTTAACTTTGAAGGGTTCACC	54075
QY	1707	AGGTGAGGAGAGTGTGGAACTGCAATTAACCTGGGAGTGTGGTGGAGTCCGATGATTC	1766
Db	54076	AGGTGAGGAGAGTGTGGAACTGCAATTAACCTGGGAGTGTGGTGGAGTCCGATGATTC	54135
QY	1767	TCCTTTGCTAAGTGCATGACATATTTTGGCTTTTATTACAGTTTATCTATGGCACCCTATG	1826
Db	54136	TCCTTTGCTAAGTGCATGACATATTTTGGCTTTTATTACAGTTTATCTATGGCACCCTATG	54195
QY	1827	CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTTGTCAGATGCTTCTTAGGCCA	1886
Db	54196	CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTTGTCAGATGCTTCTTAGGCCA	54255
QY	1887	CATCCCCCTGTCTAAAAATTCAGAAAAATTTTGGTTTATAAAGATGCATTTATCTATGATA	1946
Db	54256	CATCCCCCTGTCTAAAAATTCAGAAAAATTTTGGTTTATAAAGATGCATTTATCTATGATA	54315
QY	1947	TGCTAATATATGATATGCAATATAA 1973	
Db	54316	TGCTAATATATGATATGCAATATAA 54342	

RESULT 8  
 AAF21273  
 ID AAF21273 standard; DNA; 152740 BP.  
 XX AAF21273;  
 AC AC  
 XX XX  
 DT 14-MAR-2001 (first entry)  
 XX Human low adenosine antisense oligonucleotide related sequence #2840.  
 DE  
 XX

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

**Homo sapiens.**

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US08020.

06-APR-1999; 99US-0127958.

(UYEC-) UNIV EAST CAROLINA.

(NICE) / NICE J W:

NYCE UW,

00/ECCE/0007 / TTH

low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 1219-1254; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, such as stimulating and immunoglobulins and antibodies, antibody receptors, transcription factors, chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAP18434 to AAE21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 152740 BP; 44169 A; 32023 C; 34549 G; 41999 T; 0 other:

Query Match 98.2%; Score 1943.8; DB 21; Length 152740;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 CTGAACAGAGAAAGTGGATTGAAACAAGACGCATTTCCCGAGTACATCCACAACATGTG 86  
+ |||||  
Db 52396 CAGAACAGAGAAAGTGGATTGAAACAAGACGCATTTCCCGAGTACATCCACAACATGTG 86

Dbb  
52396 CAGAACACGAGAAGTGGATTGAACAACCACCCCTTTTCCTCCTCATATCACTCGA

QY 1167 GAGGAGCAGTTTGGATTGTTTATTAAGGAGATACAACTCTGTATATAACAACAACCT 1226  
DB 53536 GAGGAGCAGTTTGGATTGTTTATTAAGGAGATACAACTCTGTATATAACAACAACCT 53595  
QY 1227 TCAAGGGTTTGTGAACATAGAACTCTTAAGCAGGTGCCAGGAACCTCAGGGCTGT 1286  
DB 53596 TCAAGGGTTTGTGAACATAGAACTCTTAAGCAGGTGCCAGGAACCTCAGGGCTGT 53655  
QY 1287 GTGTACTAATACAGACTATGTCAACCAATGCATATCCACATGTGTCTCAGGGAATATCC 1346  
DB 53656 GTGTACTAATACAGACTATGTCAACCAATGCATATCCACATGTGTCTCAGGGAATATCC 53715  
QY 1347 AGAAAACTGTGGGTAGACATTGACTCTCCAGAAAGCTCATCTCAGCTCCCTGAAAAAT 1406  
DB 53716 AGAAAACTGTGGGTAGACATTGACTCTCCAGAAAGCTCATCTCAGCTCCCTGAAAAAT 53775  
QY 1407 GCTCATTAACCTGTGCTAATCTCTCTTTTCTAGTCTTTCATATATTTCTTCACTCAATCTC 1466  
DB 53776 GCTCATTAACCTGTGCTAATCTCTCTTTTCTAGTCTTTCATATATTTCTTCACTCAATCTC 53835  
QY 1467 TGATCTGTCAATGCTTGAATCAAGGCCAGCTGGAGTGAAGAGAAATGTGACAG. 1526  
DB 53836 TGATCTGTCAATGCTTGAATCAAGGCCAGCTGGAGTGAAGAGAAATGTGACAG 53895  
QY 1527 GCACATGAATGGAGTGGGATAGTGGGTGAGGAGGAGAGAGAG 1586  
DB 53896 GCACATGAATGGAGTGGGATAGTGGGTGAGGAGGAGAGAGAGAGAG 53955  
QY 1587 ATGAGCATGCTGAGCTTGACAAAGCAAAAGGTGAGCAAAAGGCTCACGATTCAGCCA 1646  
DB 53956 ATGAGCATGCTGAGCTTGACAAAGCAAAAGGTGAGCAAAAGGCTCACGATTCAGCCA 54015  
QY 1647 GGAGATGATGCTGCTTACGCCCTCTGCCAGCTGATTTAACTTGAAGGTTTCAAC 1706  
DB 54016 GGAGATGATGCTGCTTACGCCCTCTGCCAGCTGATTTAACTTGAAGGTTTCAAC 54075  
QY 1707 AGGTGAGGAGAGTTTGGGAACCTGCAATAACCTGGGAGTTTGGTGAGTCCGATGATTC 1766  
DB 54076 AGGTGAGGAGAGTTTGGGAACCTGCAATAACCTGGGAGTTTGGTGAGTCCGATGATTC 54135  
QY 1767 TCTTTTGCATTAAGTGCATACATATTTTCTTTTATTTACAGTTTATCTATGGCACCCATG 1826  
DB 54136 TCTTTTGCATTAAGTGCATACATATTTTCTTTTATTTACAGTTTATCTATGGCACCCATG 54195  
QY 1827 CACCTTACATTTGAATCTATGAATATCATGCTCCATGTTTCAGATGCTTCTTAGGCCA 1886  
DB 54196 CACCTTACATTTGAATCTATGAATATCATGCTCCATGTTTCAGATGCTTCTTAGGCCA 54255  
QY 1887 CATCCCTGCTCTAAAAATTCAGAAAAATTTTGTATTAAGAGATGCATTATCTATGATA 1946  
DB 54256 CATCCCTGCTCTAAAAATTCAGAAAAATTTTGTATTAAGAGATGCATTATCTATGATA 54315  
QY 1947 TGCTTAATATATGATATGCAATATAA 1973  
DB 54316 TGCTTAATATATGATATGCAATATAA 54342

## RESULT 9

ABL32334

ID ABL32334 standard; DNA; 10528 BP.

AC ABL32334;

XX ABL32334;

XX 26-MAR-2002 (first entry)

DT Human immune system associated gene SEQ ID NO: 307.

XX Human: immune system disease; cytosine methylation; antiasthmatic;

XX Human: immune system disease; cytosine methylation; antiasthmatic;

XX antiarteriosclerotic; antianemic; cytostatic; nontropic;

XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

XX antiarthritic; antidiabetic; antipsoriatic;

XX antiinflammatory; cancer; eye disease; arteriosclerosis; anemia;

XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.

OS Homo sapiens.

PN WO200200928-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP07537.

XX 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation

XX Claim 1; SEQ ID NO 307; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.

XX Sequence 10528 BP; 3072 A; 86 C; 2419 G; 4951 T; 0 other;

XX Query Match 66.3%; Score 1313; DB 24; Length 10528;

XX Best Local Similarity 79.7%; Pred. No. 0;

XX Matches 1550; Conservative 0; Mismatches 395; Indels 0; Gaps 0;

QY 29 GAACAGAGAAAGTGGATTGAACAAGGAGCGATTTCCCGAGTACATCCACACATCTGTC 88

DB 8327 GAATAGAGAAAGTGGATTGAACAAGGAGCGATTTTGTAGTATATTTATATATGTTGT 8386

QY 89 CACATCTCGTCTCGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCCACACCTT 148

DB 8387 TATATTCGTTTCGGTTTATAGAAATATTAACGAGCGGTGAAGAGTATATTTT 8446

QY 149 TTTTGATTATGATTACGCTGCTCCCTGTCATATAATTTGACGTGAAGCAAAATTTGGGCCCA 208

DB 8447 TTTTGATTATGATTACGCTGCTCCCTGTCATATAATTTGACGTGAAGCAAAATTTGGGCCCA 8506

QY 209 ACTCTGCTCGGCTCTACTCGCTGCTTCTCATCTTGGTTTGGGCAACATCTGCT 268

DB 8507 ATTTTGTGTTTTCGTTTATCGTTGTTTATTTTGGTTTGGGTAATATGTTGT 8566

QY 269 CGTCTCATCTTAATAAACTGCAAAAAGCTGAAGTCTGCTGACTGACATTTACCTGCTCAA 328

DB 8567 CGTTTATTTATTAATAAACTGCAAAAAGCTGAAGTCTGCTGACTGACATTTACCTGCTCAA 8626

QY 329 COTGGCCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTCTGCTGC 388

DB 8627 TTTGGTTATTTTGTGTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 8686

QY 389 AAATGAGTGGGCTTTGGGAATGCAATGCAAAATATTCACAGGCTCTATACATCGG 448

DB 8687 AAATGAGTGGGCTTTGGGAATGCAATGCAAAATATTCACAGGCTCTATACATCGG 8746

QY 449 TTATTTTGGCGGAATCTTCTTCTCATCTCTCTGACAAATCGATAGATAGCTGCTATTTGT 508

DB 8747 TTATTTTGGCGGAATCTTCTTCTCATCTCTCTGACAAATCGATAGATAGCTGCTATTTGT 8806

QY	509	CCATGCTGCTGTTTGCCTTTAAAGCCAGGACGGTCACCTTTGGGTGCTGACAACTGTGAT	568
DB	8807	TTATGTTGCTGTTTCTTTTAAAGATTAGGACGGTTATTTTGGGTGCTGATAAGTGTGAT	8866
QY	569	CACCTGGTGGTGGCTGCTGTTTGGTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAA	628
DB	8867	TATTTGGTGGTGGTGTGTGTTGTTTGTGTTTAGGAATTAATTTTATTAATGCTTAGAA	8926
QY	629	AGAAGATTCTGTTTATGTCGTCGGCCCTATTTTCCAGGAGTGGNAATTAATTTCCACAC	688
DB	8927	AGAAGATTGTTTATGTTTGTGCTGTTTATTTATGGTATTTGTTATTTTATAT	8986
QY	689	AATAATGAGGAACATTTTGGGGCTGTGCTCGCGCTCATCATGTCTATCTGCTACTC	748
DB	8987	AATAATGAGGAATATTTGGGGTGTGTTTGTGCTGTTTATTTATGGTATTTGTTATTC	9046
QY	749	GGGAATCCCTGAAACCCCTGCTTCGGTGTGCGAACGAGAGAAGAGGCAATAGGCGAGTGAG	808
DB	9047	GGGAATTTTGAAATTTTGTTCGGTGTGCGAACGAGAGAAGAGGTATAGGGTAGTGAG	9106
QY	809	AGTCATCTTCCACCATCATGATTGTTTACTTTCCTCTTGACCTCCCTATAAACAATCTCAT	868
DB	9107	AGTTATTTTATTAATGATGTTTATTTTCTTTTGGATTTTTTATTAATATCTGTTAT	9166
QY	869	TCTCCTGAACCGTCCAGGAATCTTCGCCCTGACTAATCTGTGAAGCACCAGTCAACT	928
DB	9167	TTTTTTGAAATATTTTGTAGGAATTTTTCGGTGTGACTAATTTGTGAAGTATTAGTTAAT	9226
QY	929	GGACCAAGCCAGCGAGTGCACAGACTCTTGGGATGACTCACTGCTGCATCAATCCCAT	988
DB	9227	GGATTAAGTTACGTAGTGATAGAGATTTTCCGGATGATTTATTTGTTGTATTAATTTTAT	9286
QY	989	CATCTATGCTTTCGTTGGGGAGAAAGTTCAGAAAGTATCTCTCGTGTCTCTCCGAAGCA	1048
DB	9287	TATTTATGTTTTCGTTGGGAGAGTTTAGAAGTATTTTTCGGTGTTCGTTTCGAAAGTA	9346
QY	1049	CATCACCAGCGCTTCTGCAACAATGTCACGTTTTCTACAGGGAGACAGTGGATGGAGT	1108
DB	9347	TATTAATTAGCGTTTTTGTAAATAATGTTTACTGTTTTATAGGAGATAGTGGATGGAGT	9406
QY	1109	GACTTCAACAAACAGCCCTTCACATGGGAGCAGGAAGTCTCGGCTGGTTTATTAACAAG	1168
DB	9407	GATTTTAAATAACGTTTTTATTGGGGAGTAGGAAGTTTCGGTGGTTTTATTAACAAG	9466
QY	1169	GGAGCAGTTTGATTTGTTTATAAGGGAGATAACAATCTGTATATAACAACAACATTC	1228
DB	9467	GGAGTAGTTTGATTTGTTTATAAGGGAGATAATAATTTGTATATAATAATAATTTT	9526
QY	1229	AAGGGTTTGTCAACAATAAGAACCTGTAAAGCAGGTGCCAGGAACCTCAGGCTGTGT	1288
DB	9527	AGGGTTTGTGTGAATAATAGAAATTTGTAAAGTAGTGTTTAGGAATTTTAGGGTGTGT	9586
QY	1289	GTACTAATACAGACTATCTCACCCAATCCATATCCAACATGTGCTCAGGGGAATATCCAG	1348
DB	9587	GTATTAATATAGATTAUGTTTATTAUGTATTAATTAATGTTTATAGGGAATAATTTAG	9646
QY	1349	AAAACTGTGGGTAGAGACTTTTGACTCTCCAGAAGCTCATCTCAGCTCCGAAAAATGC	1408
DB	9647	AAAAATTTGGGTAGAGATTTTGTATTTTATAGAAAGTTTATTTTAGTTTTTGAANAATGT	9706
QY	1409	CTCATTAACCTTGTGCTAATCCCTTTTTTCTAGTCTTCAATAATTTCTCACTCAATCTGT	1468
DB	9707	TTTATATTTTGTGTTTAATTTTTTTTTTTTTTTAGTTTTTATTAATTTTTTATTTTTTG	9766
QY	1469	ATTCGTCAATGTCTTGAAATCAAGGCCAGCTCGAGGTGAAGAAGAAATGTCACAGGC	1528
DB	9767	ATTTTGTAAATGTTTTGAAATTAAGGGTTAGTTGGAGTGAAGAAGAAATGTCATAGGT	9826
QY	1529	ACAGATGAATGGGAGTGAAGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGAGACAT	1588
DB	9827	ATAGATGAATGGGAGTGAAGGATAGTGGGGTTAGGGTTGAGAGGAGAAGGAGGAGATAT	9886
QY	1589	GAGCATGGCTGAGCCTGGACAAGACAAGAGTGAAGCAAAAGGGCTTCACGCATTCACCCAGG	1648

[illegible]

RESULT 10  
ABL32335/c

ID ABL32335 standard; DNA; 10528 BP.

XX ABL32335:

XX  
DT 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 308.

Human: immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antiangioma; cytostatic; neurotropic; neuroprotective; anti-HIV; anticoagulant; ophthalmologic; antirheumatic; antihypertic; antidiabetic; antiparasitic; antiinflammatory; cancer; eye disease; antileukostasis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene. qs.

OS Homo sapiens.

AA  
PN  
WO200200928-A2.

03-JAN-2002

XX  
PF 02-III-2001: 2001WA-FD07537

XX  
XX

PR 01-SEP-2000; 2000DE-1043826.

AA  
PA (EPIG-) EPIGENOMICS AG.

PT Olek A. Pienenbrock C Berlin v.

XX  
WDT: 2003-120000/17

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -

Claim 1; SEQ ID NO 308; 32pp + Sequence Listing; German.

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders.



CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid  
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX  
 SQ

Sequence 10528 BP; 2873 A; 86 C; 2164 G; 5405 T; 0 other;  
 Query Match 65.0%; Score 1286.4; DB 24; Length 10528;  
 Best Local Similarity 78.9%; Pred. No. 0;  
 Matches 1533; Conservative 0; Mismatches 411; Indels 0; Gaps 0;  
 QY 30 AACAGAGAAAGTGGATTGAACAGAGCGATTTCCCCAGTAGATCCACAAAGTGTGTC 89  
 DB 2201 AAAAAAAAAAATAAATAAACAAGCGATTTCCCCATACATCCACAAATATATATCC 2142  
 QY 90 ACATCTCGTCTCGGTTTATCAGAAATACCAACGAGCGGGAAGAGTACCACCTTT 149  
 DB 2141 ACATCTCGTCTCGGTTTATCAGAAATACCAACGAGCGGGAAGAGTACCACCTTT 2082  
 QY 150 TTTGATTATGATTACGGTCTCCCTGTCTATAAATTTGAGCGGAAGAAATGGGGCCCA 209  
 DB 2081 TTTAATTAATTTACGATACCTCCCTATATAAATTTAAGTAAACAATAAATTAACCCAA 2022  
 QY 210 CTCCTGCCCTCTACTCGCTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTC 269  
 DB 2021 CTCCTACCTCCGCTCTACTCGCTAATTAATTCATCTTTAATTTTATAAACAATATATC 1962  
 QY 270 GTCCCTCATCTTAATAAAGTGAAGTGTGAGTGTGACGTGACATTTACCTGTCTCAAC 329  
 DB 1961 GTCCCTCATCTTAATAAAGTGAAGTGTGAGTGTGACGTGACATTTACCTGTCTCAAC 1902  
 QY 330 CTGGCCATCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGCTCAGCTGTGCGA 389  
 DB 1901 CTAAACCATCTAATCTTTTCTTATTAATCTCTCCCATTTAATAAACAATATATC 1842  
 QY 390 AATGAGTGGGCTTTGGGAATGCAATGTGCAATTTTCCAGGCTGTATCATCTGGT 449  
 DB 1841 AATAAATAAATCTTTAAATAAATGCAATTTTCCAGGCTGTATCATCTGGT 1782  
 QY 450 TATTTTGGGGAATCTTTCTTATCATCTTCTGACATCGATAGATACCTTGGCTATGTC 509  
 DB 1781 TATTTTAAAGCAATCTTTCTTATCATCTTCTGACATCGATAGATACCTTATATC 1722  
 QY 510 CATGCTGTGCTTTAAAGCCAGGAGGCTACCTTTGGGCTGTGCAAGTGTGATC 569  
 DB 1721 CATACTATATTTACTTTTAAACCAAAACGATCACCTTTTAAATAATAAATAAATC 1562  
 QY 570 ACCTGGTGTGCTGTGTTTGTCTGTCGCCAGGAATCATCTTTACTAATGCCAGAAA 629  
 DB 1661 ACCTAATTAATACTATATTTACTTCTATCCCAAAATCATCTTTACTAATACCAAAA 1602  
 QY 630 GAAGATCTGTTTATGCTGTGGCCCTTATTTTCCAGGAGGATGGAATAATTTCCACACA 689  
 DB 1601 AAAAAATCTATATATCTAATCCCTTATTTTCCAGGAAATAAATAAATTTCCACACA 1542  
 QY 690 ATATGAGGAACATTTGGGCTGTGCTGCTGCTCATCTGTCATCTGCTACTCG 749  
 DB 1541 ATAATAAACAATTTTAAACAATTAATCTACCGCTACTCATCAATCACTACTACTCG 1482  
 QY 750 GGAATCTGAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
 DB 1481 AATATCTAAACCCCTTACTGATATCGAAACGAAAAAATAAATAAACAATAAATAA 1422  
 QY 810 GTATCTTCCACATGATTTGTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 869  
 DB 1421 ATCATCTTCCACATATATTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1362  
 QY 870 CTCCTGAACACTTCCAGGAATCTTCCGCTGTGATGCTGTAAGACCACTGCAACTG 929  
 DB 1361 CTCCTGAACACTTCCAGGAATCTTCCGCTGTGATGCTGTAAGACCACTGCAACTG 1302  
 QY 930 GACCAAGCCAGGAGTACAGAGACTCTTGGGATGACTCTGCTGATCAATCCCATC 989

DB 1301 AACCAACACGCAATTAACAAAACTCTTAAATAAATCTACTACTATCAATCCCATC 1242  
 QY 990 ATCTATGCTTGGTGGGAGAGTTCAGAGGTATCTCTCGTGTCTTTCGGAAGCAC 1049  
 DB 1241 ATCTATGCTTGGTGGGAGAGTTCAGAGGTATCTCTCGTGTCTTTCGGAAGCAC 1182  
 QY 1050 ATCACAAGCGCTCTCGCAACAATGTCAGTTCAGGAGGAGACGTGATGAGTG 1109  
 DB 1181 ATCACAAGCGCTCTCGCAACAATGTCAGTTCAGGAGGAGACGTGATGAGTG 1122  
 QY 1110 ACTTCAACAAACAGCGCTTCCACTGGGAGCAGGAGTCTCGGCTGTTTATAAAGCAG 1169  
 DB 1121 ACTTCAACAAACAGCGCTTCCACTAAAAAACAATAAATCTCGACTAATTTATAAAGCAG 1062  
 QY 1170 GAGCAGTGTGATGTTGTTTATAAGGAGATTAACATCTGTATATAAACAACATCTTCA 1229  
 DB 1061 AAACAATTAATTAATTTATAAATAAATAAATCTGTATATAAACAACATCTTCA 1002  
 QY 1230 AGGGTTTGTGAACATAGAAACCTGTAAGCAGGTGCCCAGGAACCTCAGGCTGTGTG 1289  
 DB 1001 AAATTTATAACAATAAACAATTAACAAATACCCAAACCTCAAAACTATATA 942  
 QY 1290 TACTATACAGACTATGTCAACCAATGATATCCACATGTGCTCAGGAGTATATCCAGA 1349  
 DB 941 TACTATACAAACTATATCAACCAATGATATCCACATATCTCAAAATAATCCAAA 882  
 QY 1350 AAAAAGTGGGTAGACATTTGACTCTCCAGAAAGTCTCATCTCAGTCTCTGAAAAATGCC 1409  
 DB 881 AAAAAGTGGGTAGACATTTGACTCTCCAGAAAGTCTCATCTCAGTCTCTGAAAAATGCC 822  
 QY 1410 TCATTAACCTGTGCTAATCTCTTTTCTAGTCTCTCATATAATTTCTTCACTCAATCTCTGA 1469  
 DB 821 TCATTAACCTGTGCTAATCTCTTTTCTAGTCTCTCATATAATTTCTTCACTCAATCTCTGA 762  
 QY 1470 TTTCTGCAATGCTTGAATCAAGGCGCTGAGAGTGAAGAGAAATGTGACAGGCA 1529  
 DB 761 TTTCTGCAATGCTTGAATCAAGGCGCTGAGAGTGAAGAGAAATGTGACAGGCA 702  
 QY 1530 CAGATGAAGTGGGTAGGAGTGTGGGCTCAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 1589  
 DB 701 CAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 642  
 QY 1590 AGCATGCTGAGGCTGGACAAAGAGTGAAGAGGCTCAGGATTCAGGAGGAGGAGGAGG 1649  
 DB 641 AACATAACTAAACCTTAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 582  
 QY 1650 GATGATGCTGCTTACGCCCTCTGCGAGTGTATTTAACTTGAAGGCTTCAACGAGG 1709  
 DB 581 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 522  
 QY 1710 TCAGGAGAGGTTTGGGAACCTGCAATAAATTTTGTGAGTGTGAGTGTGAGTGTGAGTGT 1769  
 DB 521 TCAAAAAAATTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCT 462  
 QY 1770 TTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829  
 DB 461 TTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402  
 QY 1830 CTTTACATTTGAAATCTATGAATATCATGCTTCAATGTTGTGAGTGTGAGTGTGAGTGTGAG 1889  
 DB 401 CTTTACATTTAAATCTATGAATATCATGCTTCAATGTTGTGAGTGTGAGTGTGAGTGTGAG 342  
 QY 1890 CCCCTGTCTAAAAATTCAGAAAAATTTTGTGTTTATAAAGATGATGATGATGATGATGATGAT 1949  
 DB 341 CCCCTGTCTAAAAATTCAGAAAAATTTTGTGTTTATAAAGATGATGATGATGATGATGATGAT 282  
 QY 1950 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973  
 DB 281 TAAAT 258



[illegible]



PS Claim 1; Page 12; 15pp; Japanese.

The present sequence encodes human monocyte chemoattractant protein 1 (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are used for the prevention and treatment of tumours and inflammatory, viral, infectious, allergic, diabetic and central nervous system diseases.

Sequence 1083 BP: 257 A: 259 C: 245 G: 322 T: 0 other; XX 50

```
Query Match      54.5%; Score 1078.2; DB 18; Length 1083;
Best Local Similarity 99.7%; Pred. No. 2.4e-302;
Matches 1080: Conservative 0; Mismatches 3; Indels 0;
```

0;

QY	81	ATGCTGTCCACATCTCGTTTCTCGGTTTATCAGAAATATCACAGAGAGGGGTGAAGAATC	140
Db	1	ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATATCACAGAGAGGGGTGAAGAATC	60
QY	141	ACCACCTTTTTCATTATGATTACGTTGCTCCCTGTGCATATAAATTTGACGTGAAGCAAAAT	200
Db	61	ACCACCTTTTTCATTATGATTACGTTGCTCCCTGTGCATATAAATTTGACGTGAAGCAAAAT	120
QY	201	GGGGCCCAACTCTCGCTCGGCTCTACTCGCTGGTGTTCATCTTTGGTTTTTGTGGGCAAC	260
Db	121	GGGGCCCAACTCTCGCTCGGCTCTACTCGCTGGTGTTCATCTTTGGTTTTTGTGGGCAAC	180
QY	261	ATGCTGGTGTCTCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCCTGACTCACATTTTAC	320
Db	181	ATGCTGGTGTCTCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCCTGACTCACATTTTAC	240
QY	321	CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTTATTACTCTCCATTTGGGGCTCAC	380
Db	241	CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTTTATTACTCTCCATTTGGGGCTCAC	300
QY	381	TCTGCTGCAAAATGAGTGGGTCCTTTGGGAATGCAATGTCAAAATTAATTCACAGGGCTGAT	440
Db	301	TCTGCTGCAAAATGAGTGGGTCCTTTGGGAATGCAATGTCAAAATTAATTCACAGGGCTGAT	360
QY	441	CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCTCTCTGCAATCATAGATACCTG	500
Db	361	CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCTCTCTGCAATCATAGATACCTG	420
QY	501	GCTATGTGCCAATGCTGTGTTTTGTTTTAAAAAGCAGAGCGTGACCTTTGGGGTGGTGACA	560
Db	421	GCTATGTGCCAATGCTGTGTTTTGTTTTAAAAAGCAGAGCGTGACCTTTGGGGTGGTGACA	480
QY	561	AGTGTGATCACTGTTTGGTGGCTGTCTTGTCTCTGCCAGGAATCATCTTTTACTATAA	620
Db	481	AGTGTGATCACTGTTTGGTGGCTGTCTTGTCTCTGCCAGGAATCATCTTTTACTATAA	540
QY	621	TGCCAGAAGAAGATTCGTGTTATGTCTGTGGGCCCTTATTTTCCAGAGGATGGAATAT	680
Db	541	TGCCAGAAGAAGATTCGTGTTATGTCTGTGGGCCCTTATTTTCCAGAGGATGGAATAT	600
QY	681	TTCCACACAATTAATGAGGAACATTTTGGGGTGTGCTCGCGTGTCTCATCATGGTTCATC	740
Db	601	TTCCACACAATTAATGAGGAACATTTTGGGGTGTGCTCGCGTGTCTCATCATGGTTCATC	660
QY	741	TGCTACTCGGGAATCCTGAAAACCCCTGCTCGGTGTGCGAAACGAGAAGAGAGCATAGG	800
Db	661	TGCTACTCGGGAATCCTGAAAACCCCTGCTCGGTGTGCGAAACGAGAAGAGAGCATAGG	720
QY	801	GGAGTGAGAGTCATCTTACCACATCATGATTTGTTTACTTTTCTTCTGACTCCCTATAAC	860
Db	721	GGAGTGAGAGTCATCTTACCACATCATGATTTGTTTACTTTTCTTCTGACTCCCTATAAT	780
QY	861	ATTGTGATCTCTCCTGAAACACCTTCCAGGAATTCCTTGGCCCTGAGTAACTGTGAAGACC	920
Db	781	ATTGTGATCTCTCCTGAAACACCTTCCAGGAATTCCTTGGCCCTGAGTAACTGTGAAGACC	840
QY	921	AGTCAACTGGACCAAGCCACGAGGTGACAGAGACTCTTTGGGATGACTCTACTGCTGATC	980
Db	841	AGTCAACTGGACCAAGCCACGAGGTGACAGAGACTCTTTGGGATGACTCTACTGCTGATC	900

QY	981	AATCCCATCATCTATGCCCTTCGTTGGGAGAAAGTTCAGAAGTATCTCTCGGTGTTCTTC	1040
Db	901	AATCCCATCATCTATGCCCTTCGTTGGGAGAAAGTTCAGAAGTATCTCTCGGTGTTCTTC	960
QY	1041	CGAAGCACATCACCAAAGCGCTTTCGAAACAATGTCAGTTTCTACAGGGAGACAGTG	1100
Db	961	CGAAGCACATCACCAAAGCGCTTTCGAAACAATGTCAGTTTCTACAGGGAGACAGTG	1020
QY	1101	GATGGAGTGACCTTCACAAACACGCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA	1160
Db	1021	GATGGAGTGACCTTCACAAACACGCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA	1080
QY	1161	TAA	1163
Db	1081	TAA	1083
RESULT	15		
AAQ96297			
CDNA	AAQ96297	standard:	cdna: 2232 BP.

RESULT 15

AAQ96297 standard: CDNA: 2232 BP.

AAO96297:

XX  
XX

DT 29-DEC-1995 (first entry)

XX  
DE  
Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX Monocyte chemoattractant protein-1 receptor: MCP-1R; chemokine: ss.

KW	Monocyte chem
XX	
OS	Homo sapiens.

CD	name	category
XX		
FH	Key	Location/Qualifiers

```

FH key
FT CDS
FT 40..1161
FT /*tag= a

```

FI  
XX  
PN W09519436-A.

PD 20-JUL-1995.

11-JAN-1995; 95WO-US00476.

13-JAN-1994: 94US-0182962;

FR 13 JAN 1964; 2405 CEC  
XX  
PA (REGC ) UNIV CALIFORNIA:

FA (REGC / UNIV CALIF ORG)  
XX  
PT Charo I. Coughlin S:

PI  
XX  
DP

DR WPI; 1993-203000/34.  
DR P-PSDB; AAR79165.  
yy

xx DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
pt PT  
xx  
pt  
pt for identifying antagonists and for treating diseases characterised by  
pt monocyte infiltrates  
xx

PT monocyctic infiltrates  
XX  
PS Disclosure: Fig 1: 84pp: English.

DISCUSSION: Fig 17, 84pp, English.

To identify and clone new members of the chemokine receptor gene family, degenerate oligo primers were designed corresp. to the conserved sequences R79167 in the second and R79168 in the third transmembrane domains of the MIP-lalpha/RANTES receptor, the IL-8 receptors and the HUMSPRS orphan receptor (GenBank Accession #M99293. The degenerate oligo incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and Q96300. Amplification of cDNA derived from MM6 cells with the primers yielded a number of PCR products. One cDNA appeared to encode a novel protein. To obtain a full-length version of this clone, a MM6 cDNA library was constructed in pFROG and probed with the PCR product. A 2.1 kb cDNA clone was obt'd. Analysis of additional clones in the MM6 cDNA library revealed a second sequence that was identical to the 2.1 kb cDNA sequence first obt'd. from the 5' UTR through the putative seventh transmembrane domain but contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl-terminal

CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA  
and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature  
CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB  
XX has a mol. wt. of about 41,000 daltons.  
SQ Sequence 2232 BP; 602 A; 464 C; 508 G; 658 T; 0 other;

Query Match 49.5%; Score 980; DB 16; Length 2232;  
Best Local Similarity 100.0%; Pred. No. 1.2e-273;  
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GGATTGAACAAGCAGCGATTCCCCAGTACATCACAAACATGCTGTCACATCTCGTTCT 101  
DB 1 GGATTGAACAAGCAGCGATTCCCCAGTACATCACAAACATGCTGTCACATCTCGTTCT 60  
QY 102 CGTTTATCAGAATACCAACGAGAGCGGTGAAGAAGTACCACCTTTTGTGATTATGAT 161  
DB 61 CGTTTATCAGAATACCAACGAGAGCGGTGAAGAAGTACCACCTTTTGTGATTATGAT 120  
QY 162 TAGGGTCTCCCTGTCTATAAATTGACGTGAAGCAAAATGGGGCCCAACTCCTGCCCTCG 221  
DB 121 TAGGGTCTCCCTGTCTATAAATTGACGTGAAGCAAAATGGGGCCCAACTCCTGCCCTCG 180  
QY 222 CTCCTACTCGTGTGTTTCATCTTTTGTGTTTGTGGCAACATGCTGCTCCTCATCTTA 281  
DB 181 CTCCTACTCGTGTGTTTCATCTTTTGTGTTTGTGGCAACATGCTGCTCCTCATCTTA 240  
QY 282 ATAACTGCAAAAGCTGAAGTGCCTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 341  
DB 241 ATAACTGCAAAAGCTGAAGTGCCTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300  
QY 342 GATCTGCTTTTCTTATTACTCTCCCATTTGTTGGGCTCACTCTCTGCAAAATGAGTGGTC 401  
DB 301 GATCTGCTTTTCTTATTACTCTCCCATTTGTTGGGCTCACTCTCTGCAAAATGAGTGGTC 360  
QY 402 TTGGGAATGCAATGTGCAAAATTTATCAGAGGCTGTATCACATCGSTTATTTTGGCGGA 461  
DB 361 TTGGGAATGCAATGTGCAAAATTTATCAGAGGCTGTATCACATCGSTTATTTTGGCGGA 420  
QY 462 ATCTTCTTCAATCATCTCTGCAATTCGATAGATACCTGGCTATTGCTCATGCTGTGTT 521  
DB 421 ATCTTCTTCAATCATCTCTGCAATTCGATAGATACCTGGCTATTGCTCATGCTGTGTT 480  
QY 522 GCTTTAAAGCCAGGACGGTCACTTTGGGGTGTGACAAGTGTGATCACCCTGGTTGGTG 581  
DB 481 GCTTTAAAGCCAGGACGGTCACTTTGGGGTGTGACAAGTGTGATCACCCTGGTTGGTG 540  
QY 582 GCTGTGTTTGTCTGTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCCTTT 641  
DB 541 GCTGTGTTTGTCTGTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCCTTT 600  
QY 642 TATGCTGTGGCCCTTATTTCCAGGAGATGGAATATTTCCACACATAATGAGGAAC 701  
DB 601 TATGCTGTGGCCCTTATTTCCAGGAGATGGAATATTTCCACACATAATGAGGAAC 660  
QY 702 ATTTGGGGCTGGRCTCGCTGCTCATATGTCATCTGCTACTCGGAAATCCTGAA 761  
DB 661 ATTTGGGGCTGGRCTCGCTGCTCATATGTCATCTGCTACTCGGAAATCCTGAA 720  
QY 762 ACCCTGCTCGGTGCGAAGCAGAAAGAGGCGATAGGGCAGTGAGAGTCACTTCCACC 821  
DB 721 ACCCTGCTCGGTGCGAAGCAGAAAGAGGCGATAGGGCAGTGAGAGTCACTTCCACC 780  
QY 822 ATCATGATTGTTTACTTCTCTCTGACTCCCTATACATTGTCATTCCTGAAACACC 881  
DB 781 ATCATGATTGTTTACTTCTCTCTGACTCCCTATACATTGTCATTCCTGAAACACC 840  
QY 882 TTCAGGAATTCCTGCGCTGAGTAACTGTGAAAGCAGCAGTCAACTGCAAGCCACG 941  
DB 841 TTCAGGAATTCCTGCGCTGAGTAACTGTGAAAGCAGCAGTCAACTGCAAGCCACG 900  
QY 942 CAGGTGACAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTC 1001  
DB 1001 CAGGTGACAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTC

Db 901 CAGGTGACAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTC 960  
QY 1002 GTTGGGAGAAAGTTCAGAAG 1021  
DB 961 GTTGGGAGAAAGTTCAGAAG 980

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